



Search  for

Limits Preview/Index History Clipboard Details

Display  Show:

1: AAD05421. NADH:ubiquinone o...[gi:4164446]

BLink, Links

LOCUS AAD05421 129 aa linear PRI 19-JAN-1999  
DEFINITION NADH:ubiquinone oxidoreductase B15 subunit [Homo sapiens].  
ACCESSION AAD05421  
VERSION AAD05421.1 GI:4164446  
DBSOURCE locus AF044957 accession [AF044957.1](#)  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM [Homo sapiens](#)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (residues 1 to 129)  
AUTHORS Loeffen,J.L., Triepels,R.H., van den Heuvel,L.P., Schuelke,M.,  
Buskens,C.A., Smeets,R.J., Trijbels,J.M. and Smeitink,J.A.  
TITLE cDNA of eight nuclear encoded subunits of NADH:ubiquinone  
oxidoreductase: human complex I cDNA characterization completed  
JOURNAL Biochem. Biophys. Res. Commun. 253 (2), 415-422 (1998)  
MEDLINE [99097250](#)  
PUBMED [9878551](#)  
REFERENCE 2 (residues 1 to 129)  
AUTHORS Triepels,R., Loeffen,J., van den Heuvel,B., Schuelke,M.,  
Buskens,C., Smeets,R., Trijbels,F. and Smeitink,J.  
TITLE Direct Submission  
JOURNAL Submitted (28-JAN-1998) Nijmegen Center for Mitochondrial  
Disorders, University Hospital Nijmegen, P.O. Box 9101, Nijmegen,  
Gelderland 6500 HB, Netherlands  
COMMENT Method: conceptual translation supplied by author.  
FEATURES  
source 1..129  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
[Protein](#) 1..129  
/product="NADH:ubiquinone oxidoreductase B15 subunit"  
/name="complex I subunit"  
[CDS](#) 1..129  
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/note="NDUFB4 subunit"  
ORIGIN  
1 msfpkykpss lrtlpetldp aeynispetr raqaerlair aqlkreyllq yndpnrrgli  
61 enpallrway artinvypnf rptpknsimg alcgfgplif iyyiikterd rkekliqegk  
121 ldrtfhlsy  
//

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[NCBI](#) | [NLM](#) | [NIH](#)

Apr 28 2003 10:17:55

SeqServer®  
biology in silico

BLAST2 Search Results

Sequences Help

Retrieval BLAST2 FASTA ClustalW GCG-Assembly Phrap Translation  
BLAST2 Manual

Confidential - Property of Incyte Genomics, Inc. SeqServer Version 4.8 Jan 2002

Program: blastp  
Sequence ID(s):

1600202CD1\_SEQIDNO:3 vs. gensept134

NCBI-BLASTP 2.0.10 (Aug-26-1999)

Reference: Altschul, Stephen P., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Query: 1600202CD1\_SEQIDNO:3  
(129 letters)

Database: gensept134  
1,315,470 sequences; 407,408,102 total letters

Searching.....done

Sequences producing significant alignments:

	Score (bits)	E Value
g4164446 NADH:ubiquinone oxidoreductase B15 subunit (Homo sapiens)	268	4e-71
g12654091 NADH dehydrogenase (ubiquinone) 1 beta subcomplex, NSPKYKSSSLRTLPETLDPAEYNTSPETRAQAERLAIRAQLREYLLQYNDNRGGLI	268	4e-71
g21961382 Unknown (protein for IMAGE:5165512) (Homo sapiens)	226	2e-58
g12858553 unnamed protein product (Mus musculus)	210	1e-53
g12844830 unnamed protein product (Mus musculus)	210	1e-53
g28189195 similar to B15 subunit of the NADH: ubiquinone oxid	204	7e-52
g114 B15 subunit of the NADH: ubiquinone oxidoreductase comp1	204	7e-52
g28189643 similar to B15 subunit of the NADH: ubiquinone oxid	147	9e-35
g12836337 unnamed protein product (Mus musculus)	94	2e-18
g517250 hypothetical protein walter (Gallus gallus)	62	4e-09

>g4164446 NADH:ubiquinone oxidoreductase B15 subunit (Homo sapiens)  
Length = 129

Score = 268 bits (678), Expect = 4e-71  
Identities = 129/129 (100%), Positives = 129/129 (100%)

Query: 1 NSPKYKSSSLRTLPETLDPAEYNTSPETRAQAERLAIRAQLREYLLQYNDNRGGLI 60

NSPKYKSSSLRTLPETLDPAEYNTSPETRAQAERLAIRAQLREYLLQYNDNRGGLI

NSPKYKSSSLRTLPETLDPAEYNTSPETRAQAERLAIRAQLREYLLQYNDNRGGLI 60

Query: 61 ENPALLRWAVARTINVTNFRPTPTNSLMGALCGFGPLIFTYIINTURKEKLIQEK 120

ENPALLRWAVARTINVTNFRPTPTNSLMGALCGFGPLIFTYIINTURKEKLIQEK

ENPALLRWAVARTINVTNFRPTPTNSLMGALCGFGPLIFTYIINTURKEKLIQEK 120

Query: 121 LQRTPHLSY 129

LQRTPHLSY

Query: 121 LQRTPHLSY 129

LQRTPHLSY

>g12654091 NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 4

(15KD, B15) (Homo sapiens)

Length = 129

Score = 268 bits (678), Expect = 4e-71

Identities = 129/129 (100%), Positives = 129/129 (100%)

Query: 1 NSPKYKSSSLRTLPETLDPAEYNTSPETRAQAERLAIRAQLREYLLQYNDNRGGLI 60

NSPKYKSSSLRTLPETLDPAEYNTSPETRAQAERLAIRAQLREYLLQYNDNRGGLI

NSPKYKSSSLRTLPETLDPAEYNTSPETRAQAERLAIRAQLREYLLQYNDNRGGLI 60

Query: 61 ENPALLRWAVARTINVTNFRPTPTNSLMGALCGFGPLIFTYIINTURKEKLIQEK 120

ENPALLRWAVARTINVTNFRPTPTNSLMGALCGFGPLIFTYIINTURKEKLIQEK

ENPALLRWAVARTINVTNFRPTPTNSLMGALCGFGPLIFTYIINTURKEKLIQEK 120

Query: 121 LQRTPHLSY 129

LQRTPHLSY

Query: 121 LQRTPHLSY 129

LQRTPHLSY

>g21961382 Unknown (protein for IMAGE:5165512) (Homo sapiens)

Length = 119

Score = 226 bits (569), Expect = 2e-58

Identities = 108/108 (100%), Positives = 108/108 (100%)

Query: 2 SPFKYKSSSLRTLPETLDPAEYNTSPETRAQAERLAIRAQLREYLLQYNDNRGGLI 61

SPFKYKSSSLRTLPETLDPAEYNTSPETRAQAERLAIRAQLREYLLQYNDNRGGLI

SPFKYKSSSLRTLPETLDPAEYNTSPETRAQAERLAIRAQLREYLLQYNDNRGGLI 60

Query: 62 NPALLRWAVARTINVTNFRPTPTNSLMGALCGFGPLIFTYIINTURKEKLIQEK 109

NPALLRWAVARTINVTNFRPTPTNSLMGALCGFGPLIFTYIINTURKEKLIQEK

NPALLRWAVARTINVTNFRPTPTNSLMGALCGFGPLIFTYIINTURKEKLIQEK 108

Query: 61 NPALLRWAVARTINVTNFRPTPTNSLMGALCGFGPLIFTYIINTURKEKLIQEK 120

NPALLRWAVARTINVTNFRPTPTNSLMGALCGFGPLIFTYIINTURKEKLIQEK

NPALLRWAVARTINVTNFRPTPTNSLMGALCGFGPLIFTYIINTURKEKLIQEK 120

Query: 121 LQRTPHLSY 129

LQRTPHLSY

Query: 121 LQRTPHLSY 129

LQRTPHLSY

>g12858553 unnamed protein product (Mus musculus)

Length = 129

Score = 210 bits (529), Expect = 1e-53

Identities = 97/129 (75%), Positives = 113/129 (87%)

Query: 1 NSPKYKSSSLRTLPETLDPAEYNTSPETRAQAERLAIRAQLREYLLQYNDNRGGLI 60

NSPKYKSSSLRTLPETLDPAEYNTSPETRAQAERLAIRAQLREYLLQYNDNRGGLI

NSPKYKSSSLRTLPETLDPAEYNTSPETRAQAERLAIRAQLREYLLQYNDNRGGLI 60

<http://patents.incyte.com:8000/cgi-bin/SeqServer/SeqServer>

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Query: 1  NSPDK+ S L +JP TUDP+VS ER+NO+BLA+R+++KREY LOY DP+RG+1
          NSPDK+BL+SS+L+PTTLD+P+D+DIS+T+NO+Q+BL+R+SL+R+K+R+O+Y+Q+Y+D+P+R+G+1 60

Query: 61  EOP+L+R+VA+NT+V+T+N+P+T+N+S+L+M+O+L+O+G+R+L+P+Y+I+I+T+R+D+R+K+L+I+O+R+K 120
          E+P+L+R+V+R+Y+R+P+R+K X S+L+O+L G G+R+L P Y+ R+T+R+D+R+K+L+I+O+R+K

Query: 61  EOP+L+R+V+T+V+R+S+N+I+P+R+P+N+K+S+L+O+L+G+I+G+V+P+V+Y+P+T+R+D+R+K+L+I+O+R+K 120

Query: 121  LKRT+H+L+Y 129
          LKRT+H+SY

Query: 121  LKRT+H+L+Y 129

```

>Q281896643 similar to B15 subunit of the NADH: ubiquinone  
oxidoreductase complex [Bos taurus]

Score = 147 bits (368), Expect = 9e-35  
 Identities = 68/97 (71%) Positives = 82/97 (84%)

Query: 1  
MSPPKVESSILPTITPTLPDPAKINISPPETROAVERLITMOUKERLLOYNDAIRBGLI 60  
MSPPKRY + S L +LP TLDPAR+IS ETR+AOVERLAIN++LAREY LOY DP+RRC+1  
MSPPKRYEYIYET COT DORRY TOLIPKICETEMVYDIAI EYU 1 TSCU KUDUN/ONYMORCIG 60

Query: 61 ENPALLRNAVARTINYNFRPTTNSIMGLCGRGP 97  
E+PL+RW VAR+ N+YNCRP K SL+GL GP

cg12836537 unnamed protein product (Mus musculus)

Score = 93.6 bits (229), Expect = 2e-18  
Identities = 44/56 (78%), Positives = 49/56 (85%)

MS KKKP+ L TLP TLDPAEY++SPETRAAQ ERL+IRA+LKREYTLQYNDP R  
Sbjct: 1 MGSKKYKPAPLATLPSTLDPAEYDVSPTETRAQVERLSIRARLKREYTLQYNDPQR 56

~~g512250~~ hypothetical protein walter (Gallus gallus)  
length = 179

Score = 62.5 bits (149), Expect = 4e-09  
Identities = 30/50 (60%), Positives = 38/50 (76%)

Sejce: 26 EVRPNKVVSLPAELDPAITYDTPLEKRBAAERLALIRALIKQYLLQLNTP 75

Posted date: Feb 28, 2003 2:38 PM  
Number of letters in database: 407,408,102  
Number of sequences in database: 1,315,470

Lambda	K	H
0.321	0.140	0.416

BLAST2 Results

Lambda K H  
0.270 0.0470 0.230

Matrix: BLOSUM62  
Gap Penalties: Existence: 11, Extension: 1  
Number of Hits to DB: 110103617  
Number of Sequences: 1315470  
Number of extensions: 4259804  
Number of successful extensions: 7863  
Number of sequences better than 10.0: 17  
Number of HSP's better than 10.0 without gapping: 15  
Number of HSP's successfully gapped in prelim test: 2  
Number of HSP's that attempted gapping in prelim test: 7848  
Number of HSP's gapped (non-prelim): 17  
length of query: 129  
length of database: 407,408,102  
effective HSP length: 52  
effective length of query: 77  
effective length of database: 339,003,662  
effective search space: 26103281974  
effective search space used: 26103281974  
T: 11  
A: 40  
X1: 16 (7.4 bits)  
X2: 38 (14.8 bits)  
X3: 64 (24.9 bits)  
S1: 41 (21.8 bits)

Submit sequences to:

